

FIG. 1

1	MSLSSPGVHLYFYDSRGGAGALDELCEWGLEEQGVPCQA	IT	Majority
1	MSLSSPGVHLYFYHSRWQGT	RVLD	ELC
1	MSLSSPPGVRLFYDPRGHAGAI	NE	LC
	YDGGGDA	AA	LG
	CDDHDCAL	AL	GK
41	YDGGGDA	AA	LG
41	ADAA	LA	TG
81	EDRALV	CG	HT
81	ADAP	LA	TG

FIG. 4

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Aff IV
 Sca I
 ATGAAAGATCAAAACGATTTCAGTACTGGCCCCAGCGCCCGTCAATCAGGACGGGCTGATTGGCGAGTGGCCTGAAGAGGGGCTGATC 90
 TACITTTCTAGTTTTGCTAAACGTCATGACCGGGTCCGGGGCAGTTAGTCTGCGCCGACTAACCGCTCACCGGACTTCTCCCGACTAG
 M K R S K R F A V L A Q R P V N Q D G L I G E W P E E G L I
 dhaB1
 GCCATGGACAGCCCCCTTGACCCGGTCTCTCAGTAAAGTGGACAACGGTCTGATCGTGAACCTGGACGGCAACCGCCGGGACCAGTTT 180
 CGGTACCTGTCCGGGAACTGGGCCAGAGAAGTCATTTTACCCTGTTGCCAGACTAGCAGCTTGACCTGCCGTTTGGGGCCCTGGTCAAA
 A M D S P F D P V S S V K V D N G L I V E L D G K R R D Q F
 dhaB1
 Psp1406 I
 GACATGATCGACCGATTATCGCCGATTACGGGATCAACGTTGAGCGCACAGAGCAGGCAATGCCCTGGAGGCGGTGGAAATAGCCCGT 270
 CTGTACTAGCTGGCTAAATAGCGGCTAATGCGCTAGTTGCAACTCGGTGTCCTCGTTACGGGGACCCTCCGCCACCTTTATCGGGCA
 D M I D R F I A D Y A I N V E R T E Q A M R L E A V E I A R
 dhaB1
 ATGCTGGTGGATATTCAGCTCAGCCGGGAGGAGATCATTTGCCATCATTACGCCCATCAGCCGGCCAAAGCGGTCGAGGTGATGGCGCAG 360
 TAGCACCACTATAAGTGCAGTCGGCCCTCCTCTAGTAACGGTAGTGCGGGTAGTGCGGGCCGGTTTCGCCAGCTCCACTACCGCGTC
 M L V D I H V S R E E I I A I T T A I T P A K A V E V M A Q
 dhaB1

FIG..2A-1

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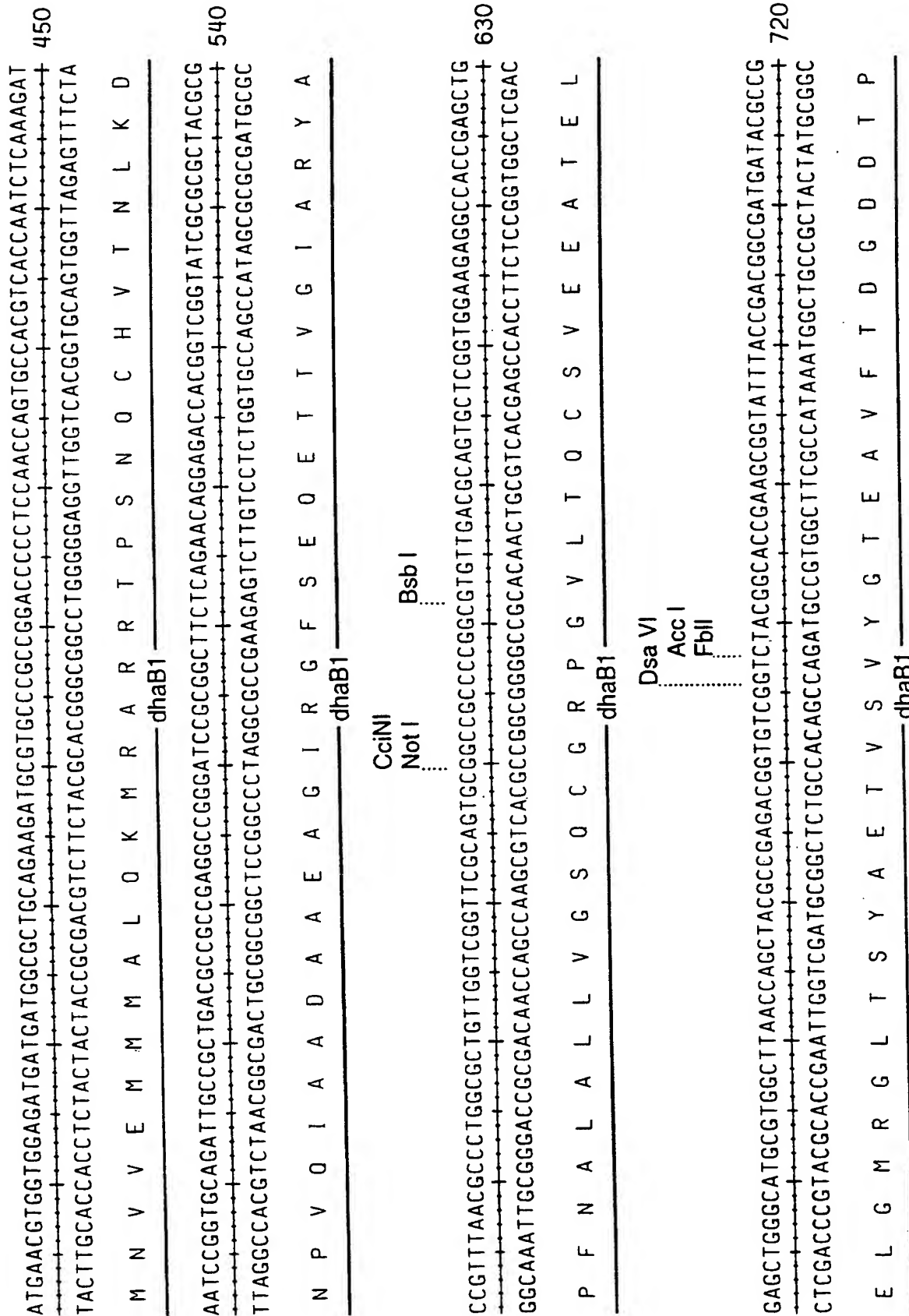


FIG._2A-2

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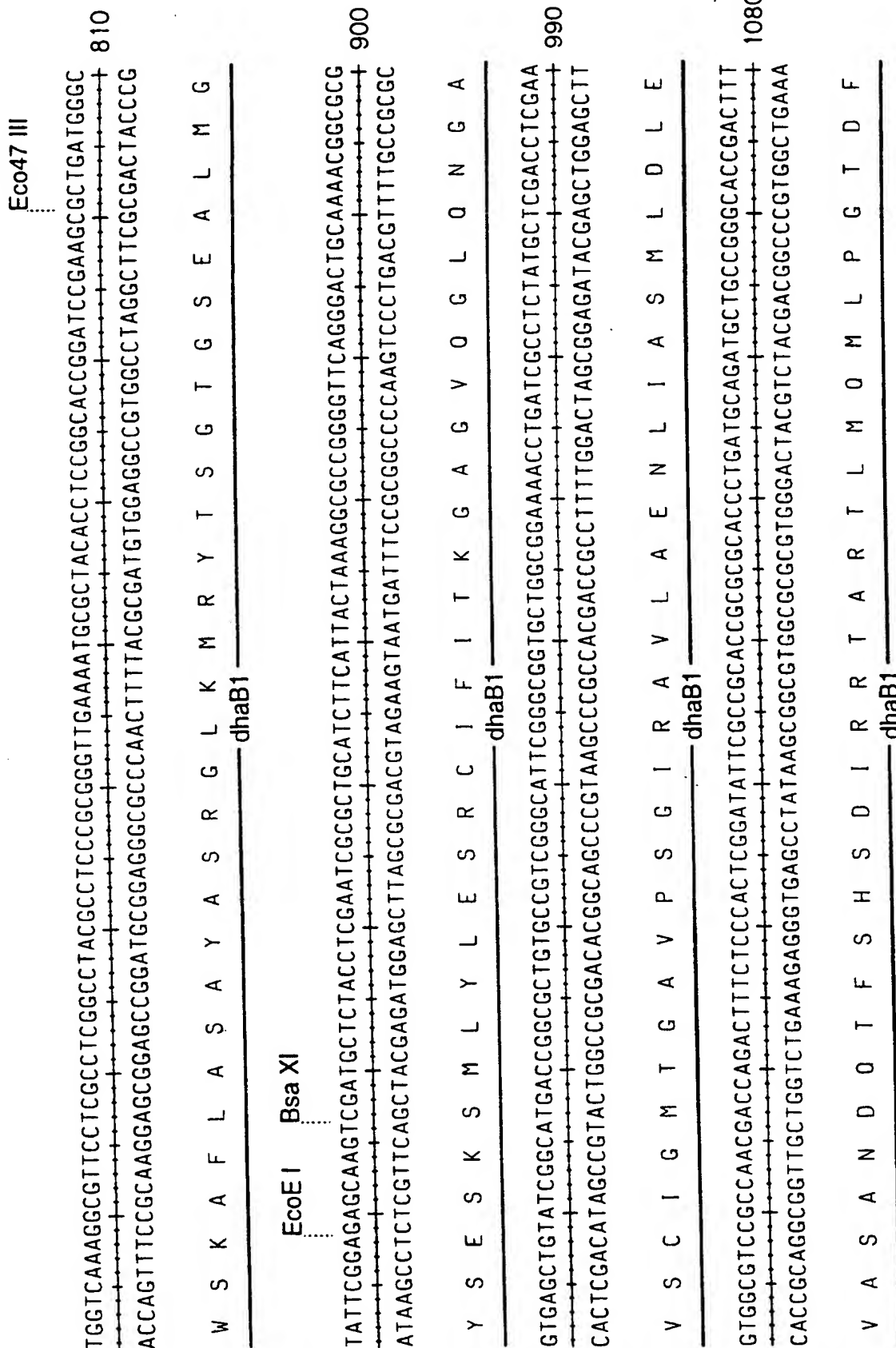


FIG. 2B-1

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P111108 I

ATTTTCTCCGGCTACAGCGGGTGCCGAACACGACAACATGTTCCGCCGGCTCGAACTTCGAATCGGAAGATTTTGATGATTACAACATC
 TAAAGAGGCCGATGTCGCCCCACGGCTTGATGCTGTTGTACAAGCGGCCGAGCTTGAAGCTACGCCCTTCTAAAACACTACTAATGTTGTAG
 1170

I F S G Y S A V P N Y D N M F A G S N F D A E D F D D Y N I
 dhaB1

CTGCAGCGTGACCTGATGGTTGACGGGGGCTGCGTCCGGTGACCGAGCGGGAACCATTTGCCATTCGCCAGAAAGCGCGGGCGGATC
 GACGTCCACITGGACTACCAACTGCCCGCGGACGCGAGCCACTGGCTCCGCTTTGGTAACGGTAAGCGGCTTTTCGCCGCGCCCGCTAG
 1260

L O R D L M V D G G L R P V T E A E T I A I R Q K A A R A I
 dhaB1

CAGCGGGTTTCCCGGAGCTGGGGCTGCCGCCCAATCGCCGACGAGGAGGTGGAGGCCGCCACCTACGCGCACGGCAGCAACGAGATGCCG
 GTCCGCCAAAAGGCGCTCGACCCCGACGGCGGTAGCGGCTGCTCTCCACCTCCGCGGGTGGATGCGCGTGCGGTCGTTGCTCTACGGC
 1350

Q A V F R E L G L P P I A D E E V E A A T Y A H G S N E M P
 dhaB1

CCGCGTAACGTGGAGGATCTGAGTCCGGTGAAGAGATGATGAAGCGCAACATCACCAGCCCTCGATATGTCGGCGCGCTGAGCCGC
 GCGCATTCACCCACCTCCTAGACTCAGCCACCTTCTCTACTACTTCCGCTTGTAGTGGCCGGAGCTATAACAGCCCGCGGCGACTCGGCG
 1440

P R N V V E D L S A V E E M M K R N I T G L D I V G A L S R
 dhaB1

FIG.-2B-2

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AGCGGCTTTGAGGATATCGCCAGCAATATTCICAATATGCTGCGCCAGCGGGTCACCGGGGATTACCTGCAGACCTCGGCCATTCTCGAT 1530
TCGCCGAAACTCCTATAGCGGTCGTTATAAGAGTTATACGACGCGGTGCGCCAGTGCGCCGCTAATGGACGCTCTGGAGCCGGTAAGAGCTA
S G F E D I A S N I L N M L R O R V T G D Y L Q T S A I L D
-----dhaB1

FIG. 2B-3

CGGCAGTTCGAGGTGGTGAGTGGGTCAACGACATCAATGACTATCAGGGGCGGGCACC GGCTATCGCATCTCTGCGCAACGCTGGGCG 1620
GCCGTCAAGCTCCACCACTCAGCCAGTTGCTGTAGTTACTGATAGTCCCCGGCCCCGTGGCCGATAGCGTAGAGACGGCTTGGACCCCGC
R Q F E V V S A V N D I N D Y O G P G T G Y R I S A E R W A
-----dhaB1

Drd II

GAGATCAAAAATATTCGGGGCGTGGTTCAGCCCGACACCATTTGAATAAGCGGGTATTCTGTGCAACAGACAAACCCAAATTCAGCCCTCT 1710
CTCTAGTTTTTATAAGGCGCCGACCAAGTCGGGCTGTGGTAACCTATTCCGCCATAAGGACACGTTGCTGTGTTGGGTTAAGTCGGGAGA
E I K N I P G V V O P D T I E
-----dhaB1

H_{dh}

V Q O T T Q I O P S
-----dhaB2

TTTACCCTGAAAACCCGCGAGGGCGGGTAGCTTCTGCCGATGAACGCGCCGATGAAGTGGTGATCGGCGTCGGCCCTGCCCTTCGATAAA 1800
AAATGGGACTTTTGGGCGCTCCCGCCCCCATCGAAGACGGCTACTTGGCGGGCTACTTCACCACTAGCCGACGCGGGACGGAAGCTATTT
F T L K T R E G G V A S A D E R A D E V V I G V G P A F D K
-----dhaB2

FIG. 2C-1

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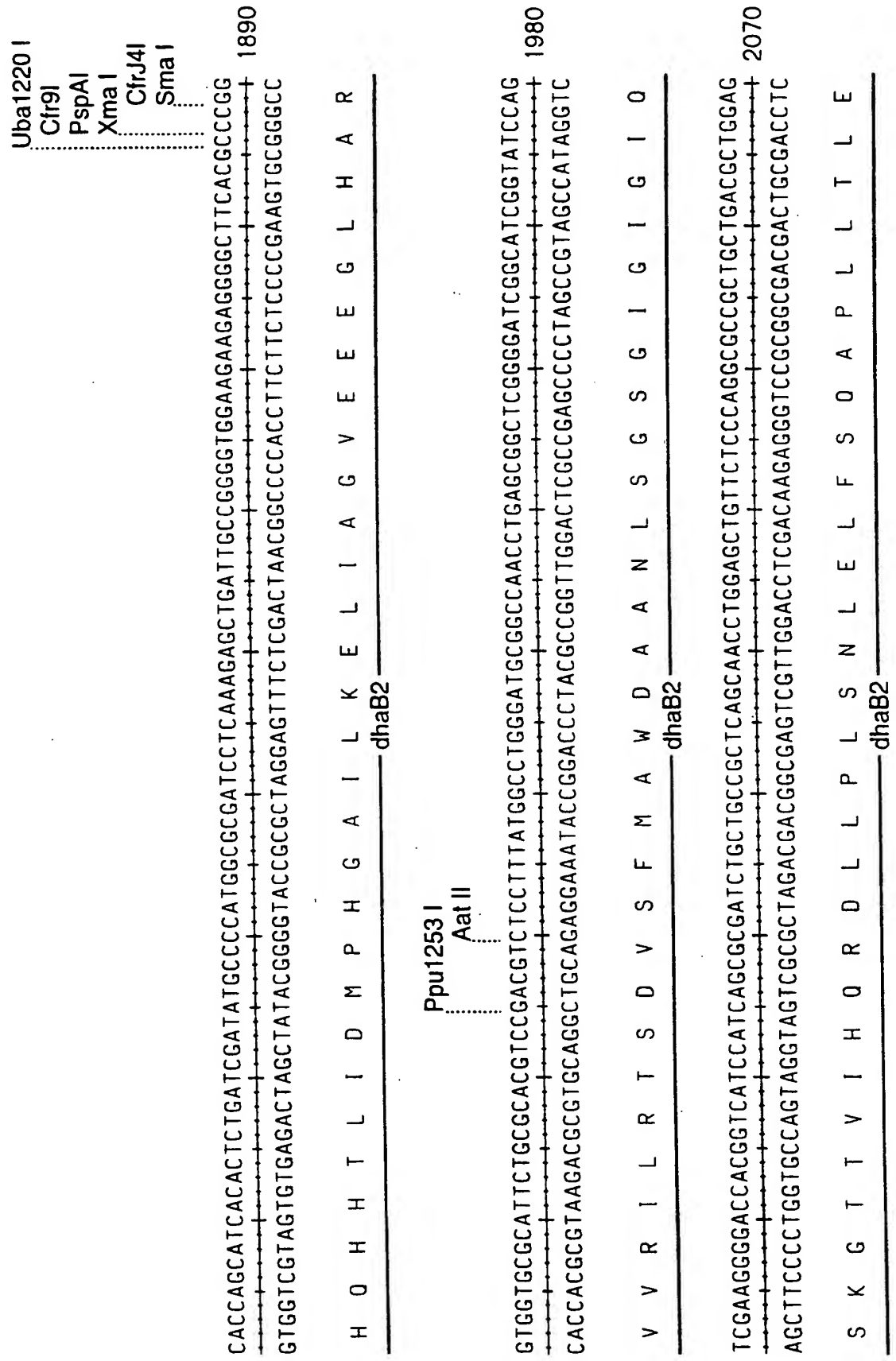


FIG.-2C-2

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ACCTACCGGCAGATTGGCAAAAACGCTGCGGCTATGCGGCAAGAGTCACCTTCGCCGGTGCCGGTGGTGAACGATCAGATGGTGCGG 2160
TGGATGGCCGCTAACCCTTTTGGGACGCGCGGATACGCGGTTTCTCAGTGGAAGCGGCCACGGCCACCACCTTGCTAGTCTACCACGCC
T Y R Q I G K N A A R Y A R K E S P S P V V N D Q M V R
-----dhaB2

FIG._2C-3

CCGAAATTTATGGCCAAAGCCGGCTATTTCATATCAAGAGACCAACATGTGTGCAGGACGCCGAGCCCGTCACCCCTGCACATCGAC 2250
GGCTTTAAATACCGGTTTCGGCGCGGATAAAGTATAGTTTCTCTGGTTGTACACCACGTCCTGCGGCTCGGGCAGTGGGACGTTGTAGCTG
P K F M A K A A L F H I K E T K H V V O D A E P V T L H I D
-----dhaB2

TTAGTAAGGAGTGACCATGAGCGAGAAAACCATGCGGTCGAGGATTATCCGTTAGCCACCCCGTCGCCGAGCATATCCTGACGCCCTA 2340
AATCATCCCTCACTGGTACTCGCTCTTTTGGTACGCGCACGTCCTAATAGGCAATCGGTGGCGGACGGGCCCTCGTATAGGACTGCGGAT
M S E K T M R V O D Y P L A T R C P E H I L T P
-----dhaB3

L V R E
-----dhaB2

FIG._2D-1

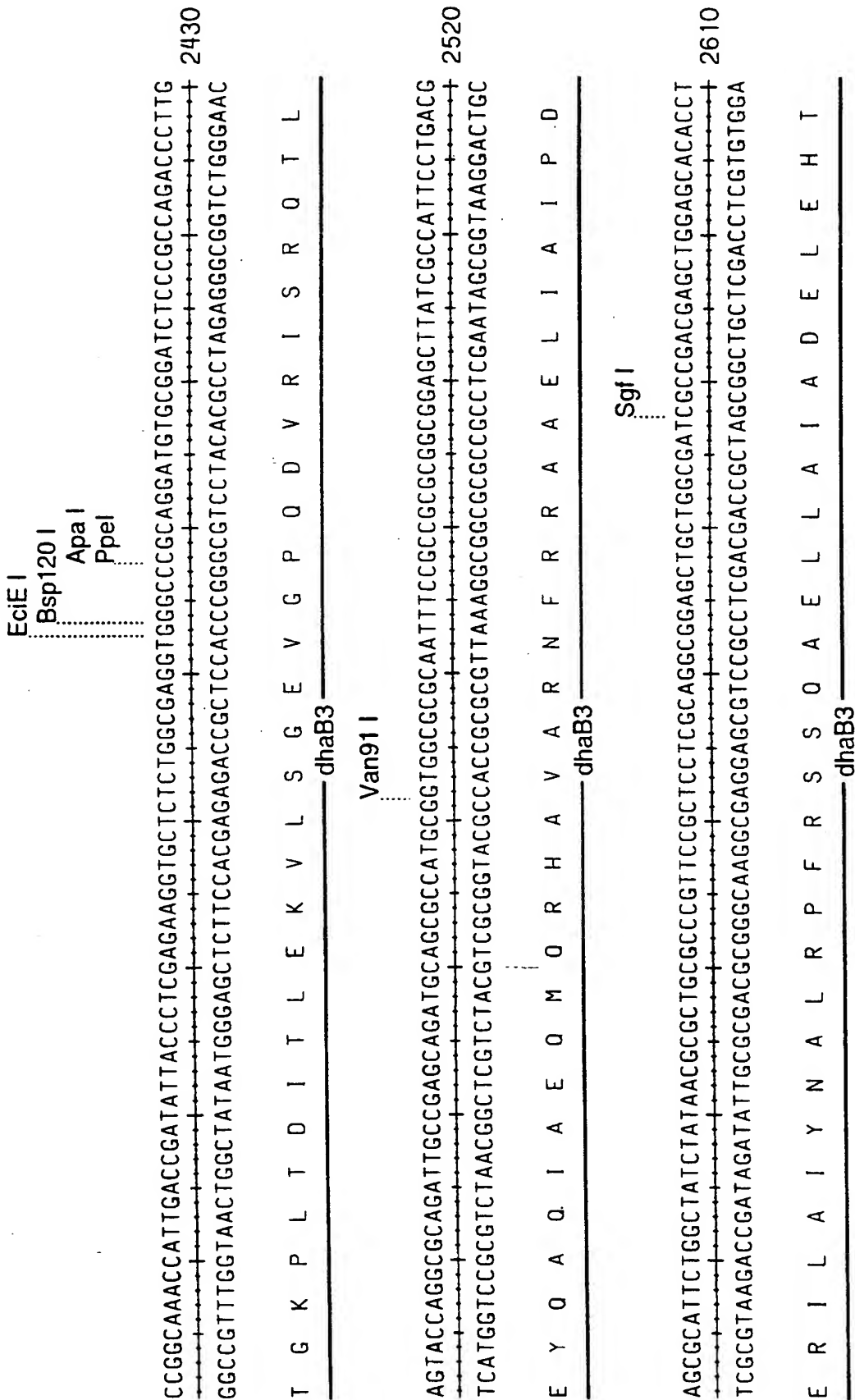


FIG._2D-2

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GGCATGCGACAGTGAATGCCGCCCTTTGTCCGGGAGTCGGCGGAAGTGATCAGCAGCGGCATAAAGCTGCGTAAAGGAAGCTAAGCGGAGG 2700
CCGTACGCTGTCACITACGGCGGAAACAGGCCCTCAGCCGCTTACACATAGTCGTGCGCGTATTCGACGCATTTCCTTCGATTCCGCTCC
W H A T V N A A F V R E S A E V Y O Q R H K L R K G S
dhaB3

Xcm I

TCAGCATGCCGTTAATAGCCGGGATTGATATCGGCAACGCCACCACCGAGGTGGCGCTGGCGTCCGACTACCCGCAGCGGAGGGCGTTTG 2790
AGTCGTACGGCAATTATCGGCCCTAACTATAGCCGTTGCGGTGGTGGCTCCACCGGACCGCAGGCTGATGGGCGTCCGCTCCCGCAAAC
M P L I A G I D I G N A T T E V A L A S D Y P Q A R A F
dhaB4

FIG..2D-3

SanD I

TTGCCAGCGGGATCGTCGCGACGACGGGCGATGAAGGGACGCGGGACAATATCGCCGGGACCCCTCGCCGCGCTGGAGCAGGCCCTGGCGGA 2880
AACGGTCGCCCTAGCAGCGCTGCTGCCCGTACTTTCCCTGCGCCCTGTTATAGCGGCCCTGGGAGCGCGGACCTCGTCCGGGACCGCT
V A S G I V A T T G M K G T R D N I A G T L A A L E O A L A
dhaB4

AAACACCGTGGTCGATGAGCGATGCTCTCGCATCTATCTTAACGAAGCCGCGCGGIGATGGCGATGIGGAGACCAITACCGG 2970
TTTGTGCCACCAGCTACTCGCTACAGAGAGCGTAGATAAGATTGCTTCGGCGGGCCCACTAACCGCTACACCGCTACCTCTGGTAGTGGC
K T P W S M S D V S R I Y L N E A A P V I G D V A M E T I T
dhaB4

FIG..2E-1

AGACCATTATCACCGAATCGACCATGATCGGTCTAATCCCGCAGACGCCGGGGGTGGCGTTGGCGTGGGACGACTATCGCCCTCG
TCCTGTAATAGTGGCTTAGCTGGTACTAGCCAGTATTGGGGCTCTCGGGCCCGCCCCACCCGCAACCGCACCCCTGCTGTATAGCGGGAGC

ETIITESTMIGHNPTPGVGVGTTIAL

dhaB4

Drd !

GGCGGCTGGCGACGCTGCCGGGGCGCAGTATGCCGAGGGTGGATCGTACTGATTGACGACGCCGTCGATTTCTTGACGCCGTGTGGT
3150
CCGGCCGACCGCTGCGACGGCGCCGGCTCATACGGCTCCCACTAGCATGACTAACTGCTGGGGCAGCTAAAGGAAC TGCGGCACACCA

G R L A T L P A A Q Y A E G W I V L I D D A V D F L D A V W

dhaB4

GGGCTCAATGAGGCGCTCGACCGGGGATCAACGTGGTGGCGGCGATCCTCAAAAGGACGACGGCGTCTGGTGACAACCGCCTGCGTA
CCCGAGTTACTCCGGGAGCTGGCCCCCTAGTTGCACCACCGCGCTAGGAGTTTTCTGCTGCCGCACGACCACCTGTTGGCGGACGCAT 3240

W L N E A L D R G I N V V A A I L K K D D G V L V N N R L R

dhaB4

Ecobi

AAACCC TCCCGTGGATGAAGTGACGCTGCTGGAGCAGGTCCCCGAGGGGGTAA TGGCGGCGGTGGAAAGTGGCCGCGCCGGGCCAGG
TTTGGGACGGCCACCACCTACTTCAC TGCGACGACCTGCTCCAGGGGCTCCCCCAT TACCGCCGCCACCTTCACCGGCGGCGCCCGGTCC 3330

K T L P V V D E V T L L E Q V P E G V M A A V E V A A P G O

dhaB4

FIG. 2E-2

3420

TGGTGGGATCCTGTCGAATCCCTACGGGATCGCCACCTTCTTCGGGCTAAGCCCGGAAGAGACCCAGGCCATCGTCCCCATCGCCCCGCG
ACCACGCTAGGACAGCTTAGGGATGCCCCTAGCGGTGAAGAAGCCGATTCGGGCTTCTCTGGGTCGGTAGCAGGGGTAGCGGGGCGC

V V R I L S N P Y G I A T F F G L S P E E T O A I V P I A R

dhaB4

3510

CCCTGATTGGCAACCGTTCGGGGTGGTGTCAAGACCCCGCAGGGGATGTGCAGTCGCGGGTGATCCCGGGGCAACCTCTACATTA
GGGACTAACCGTTGGCAAGGCGCCACACGAGTTCTGGGGCGTCCCCCTACACGTCAGCGCCCTAGGGCCGCCCTTGGAGATGTAAT

A L I G N R S A V V L K T P Q G D V O S R V I P A G N L Y I

dhaB4

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3600

GCGCGAAAGCGCGGAGAGGCGCGATGTTCGCGGAGGGCGGGAAGCCATCATGCAGGCGATGAGCGCTCGGCTCCGGTACGCGACA
CGCGCTTTTCGCGGCGCTCTCCGGCTACAGCGGCTCCCGCGCTTCGGTAGTACGTCGCGCTACTCGCGACGCGAGGCCCATGCGCTGT

S G E K R R G E A D V A E G A E A I M O A M S A C A P V R D

dhaB4

FIG..2E-3

Taq II'

3690

TCCGCGGGAACCGGACCCACGCGGCGGCAATGCTTGAGCGGTGCGCAAGGTAATGGCGTCCCTGACCGGCCATGAGATGAGCGCGA
AGGCGCGCTTGGCCCGTGGGTGCGGCGCGCGTACGAACCTCGCCACCGCTTCCATTACCGCAGGGACTGGCCGTACTCTACTCGCGCT

I R G E P G T H A G G M L E R V R K V M A S L T G H E M S A

dhaB4

FIG..2F-1

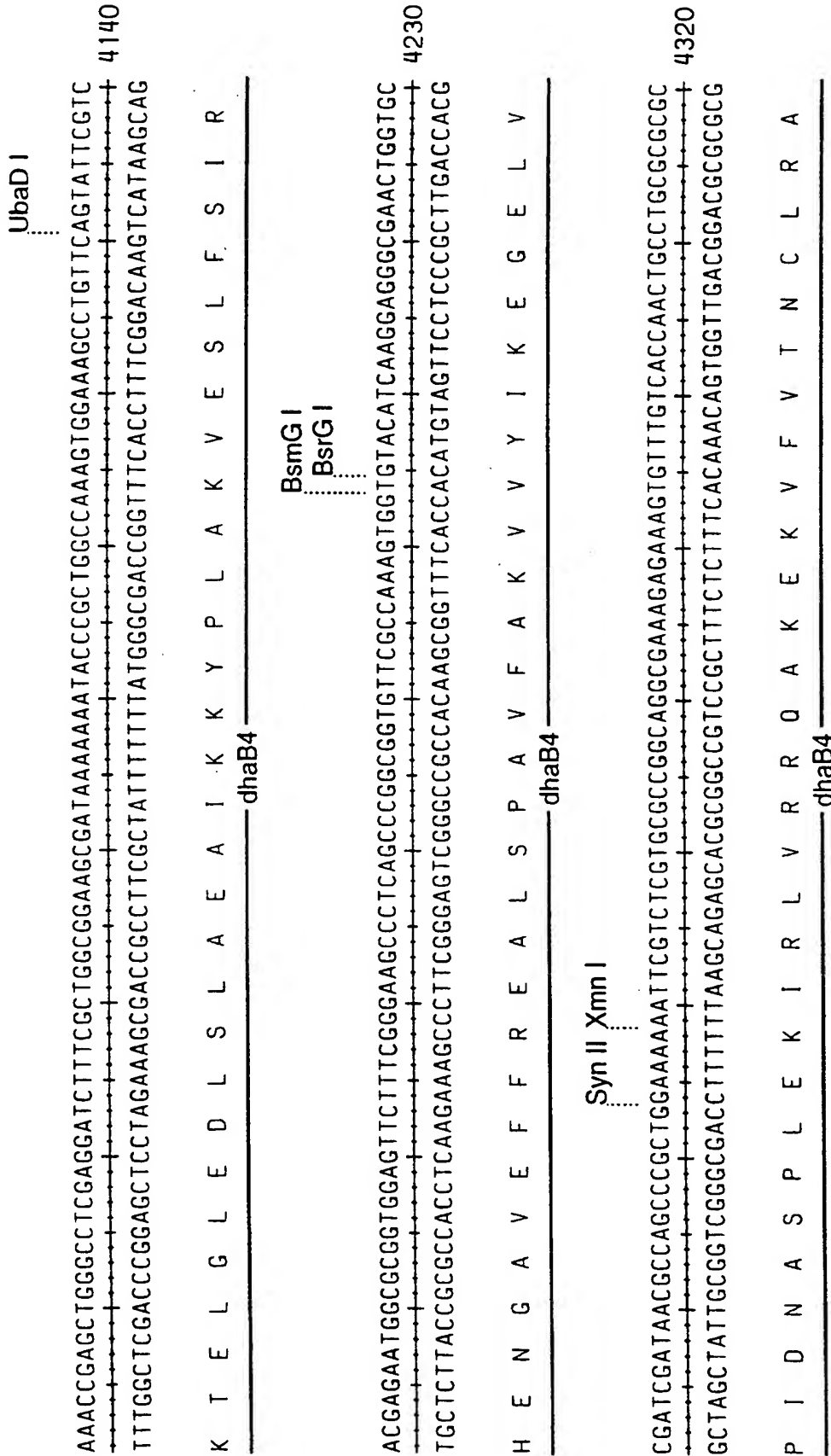
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TATACATCCAGGATCTGCTGGCGTGGATACGTTTATTCGCGCAAGGTGCAGGGCGGGATGGCCGGCGAGTGGCCCATGGAGAATGCCG 3780
 ATATGTAGGTCCTAGACGACCGCCACCTATGCAATAAGGCGGTTCCACGTCCCGCCCTACCGCGGCTCAGCGGTACCTCTTACGGC
 I Y I Q D L L A V D T F I P R K V Q G G M A G E C A M E N A
 -----dhaB4-----
 TCGGGATGGCGGCGATGGTGAAAGCGGATCGTCTGCAATGCAGGTTATCGCCCGGGAACCTGAGGCGCCGACTGCAGACCGAGGTGGTGG 3870
 AGCCCTACCGCGCGTACCACCTTCGCCCTAGCAGACGTTTACGTCCAATAGCGGGCGCTTGACTCGCGGGCTGACGCTCTGGCTCCACCACC
 V G M A A M V K A D - R L Q M Q V I A R E L S A R L Q T E V V
 -----dhaB4-----
 TGGCGGCGTGGAGGCCAACATGGCCATCGCCGGGCGTTAACCACCTCCCGGCTGTGCGGCGCGCTGGCGATCCTCGACCTCGGCGCGCG 3960
 ACCCGCCGACCTCCGGTTGTACCGGTAGCGGCGCCCGCAATTGGTGAGGGCCGACACGCCCGCGGCGCTAGGAGCTGGAGCCGCGCG
 V G G V E A N M A I A G A L T T P G C A A P L A I L D L G A
 -----dhaB4-----
 GCTCGACGGATGCGGCGATCGTCAACGCGGAGGGGCAGATAACGGCGGTCCATCTCGCCGGGCGGGGAATATGGTCAGCCTGTGATTA 4050
 CGAGCTGCCTACGCGCGTAGCAGTTGCGCCTCCCGGCTATTTGCCGCCAGGTAGAGCGGCGCCCGCCCTTATACCAGTCGGACAACTAAT
 G S T D A A I V N A E G Q I T A V H L A G A G N M V S L L I
 -----dhaB4-----

SdiI
 SfiI
 BsaK I
 BstHPI
 Hpa I

FIG.--2F-2

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TGCGCCAGGTCACCCGGGGTCCATTCGGGATATCGCCTTTGIGGTGCTGGTGGCGGCTCATCGCTGGACTTTGAGATCCCGCAGC
ACGCGTCCAGAGTGGCCCGCCCAAGTAAGCGCTATAGCGGAAACACCACGACCACCCCGCGAGTAGCGACCTGAAACTCTAGGGCGTCCG 4410

L R Q V S P G G S I R D I A F V V L V G G S S L D F E I P O
dhaB4

EcoPrr I

Bcg I'

TTATCAGGAAGCCTTGTCGCACTATGGCGTGGTCGCCGGGCAGGGCAATATTCGGGGAACAGAGGGCCCGGCAATGCGGTCCGACCCG
AATAGTGCCCTTCGGAACAGCGTGATACCGCACCGGCCCGTCCCGTTATAAGCCCCCTTGTCCTCCCGCGCGTTACGCCAGCGGTGGC 4500

L I T E A L S H Y G V V A G O G N I R G T E G P R N A V A T
dhaB4

Bcg I

GGCTGCTACTGGCCGGTCAGGCGAATTAA 4529
CCGACGATGACCGGCCAGTCCGCTTAATT

G L L L A G O A N
dhaB4

FIG. 2G

11	MMNKSQQVATITTLAAQAQMAAAVEAKALEINVA VVFSVVD	Majority
1	M - NKSQQIATITLAAAKKMAQAQAVEAKALEINVPV VFSVVD	cfu_orfY.aa
1	MMNKSQQVQTITLAAQAQMAAAVEKKATEINVA VVFSVVD	Kpn_orfY.aa
	HGGNTLLIQRMDDAFVSSCDISLNKAYSACSLKQGGTHEIT	Majority
40	HGGNTLLMQRMDDAFVTSDDISLNKAYTACCLRQGGTHEIT	cfu_orfY.aa
41	RGGNTLLIQRMDEAFVSSCDISLNKAWSAACSLKQGGTHEIT	Kpn_orfY.aa
	SAVQPPGASLYGLQLTNQQRI VIFGGGLPVI L NGQVIGAVG	Majority
80	DAVQPPGASLYGLQLTNQQRI VIFGGGLPVI L NGKVIGAVG	cfu_orfY.aa
81	SAVQPPGQSLYGLQLTNQQRI IIFGGGLPVI FNEQVIGAVG	Kpn_orfY.aa
	VSGGTVEQDQLLAETALDCFSAL	Majority
120	VSGGTVEQDRLLAETALDCFSAL	cfu_orfY.aa
121	VSGGTVEODOLLAQCALDCFSAL	Kpn_orfY.aa

FIG. 3

	MYRIYTRTGDNNGTTALFGGSSRIDKDDIRVEAYGTVDELIS	Majority
	10 20 30 40	
1	MYRIYTRTGDNNGTTALFGGSSRIDKDDIRVEAYGTVDELIS	cfu_orfW.aa
1	MYRIYTRTGDKGTTALYGGSSRIEKKDHIRVEAYGTVDELIS	kpn_orfW.aa
	QLGVCYASTRDAGLRESLHAIQQTLFVLGAELASDAKGLT	Majority
	50 60 70 80	
41	QLGVCYASTRQAELRQELHAMQKMLFVLGAELASDQKGLT	cfu_orfW.aa
41	QLGVCYATTRDAGLRESLHHIQQTLFVLGAELASDARGLT	kpn_orfW.aa
	RLSQTI GEEEDI TALEQLIDRNMAESGPKKEFVIPGKNLAS	Majority
	90 100 110 120	
81	RLKQRI GEEEDI QALEQLIDRNMAQSGP LKEFVIPGKNLAS	cfu_orfW.aa
81	RLSQTI GEEEDI TALERLIDRNMAESGPKKQFVIPGRNLAS	kpn_orfW.aa
	AQLHVARTLSRRRLERLLIAMGRALTLRDAAKRYINRLSDA	Majority
	130 140 150 160	
121	AQLHVARTLTSRRRLERILLIAMGRALTLRDAAKRYINRLSDA	cfu_orfW.aa
121	AQLHVARTQSSRRRLERLLTAMDRAHPLRDALKRRYSNRLSDA	kpn_orfW.aa
	LFSMARIEETTPDACA -	Majority
	170	
161	LFSMARIEETTPDVCA	cfu_orfW.aa
161	LFSMARIEETTRPDACA .	kpn_orfW.aa

FIG._5

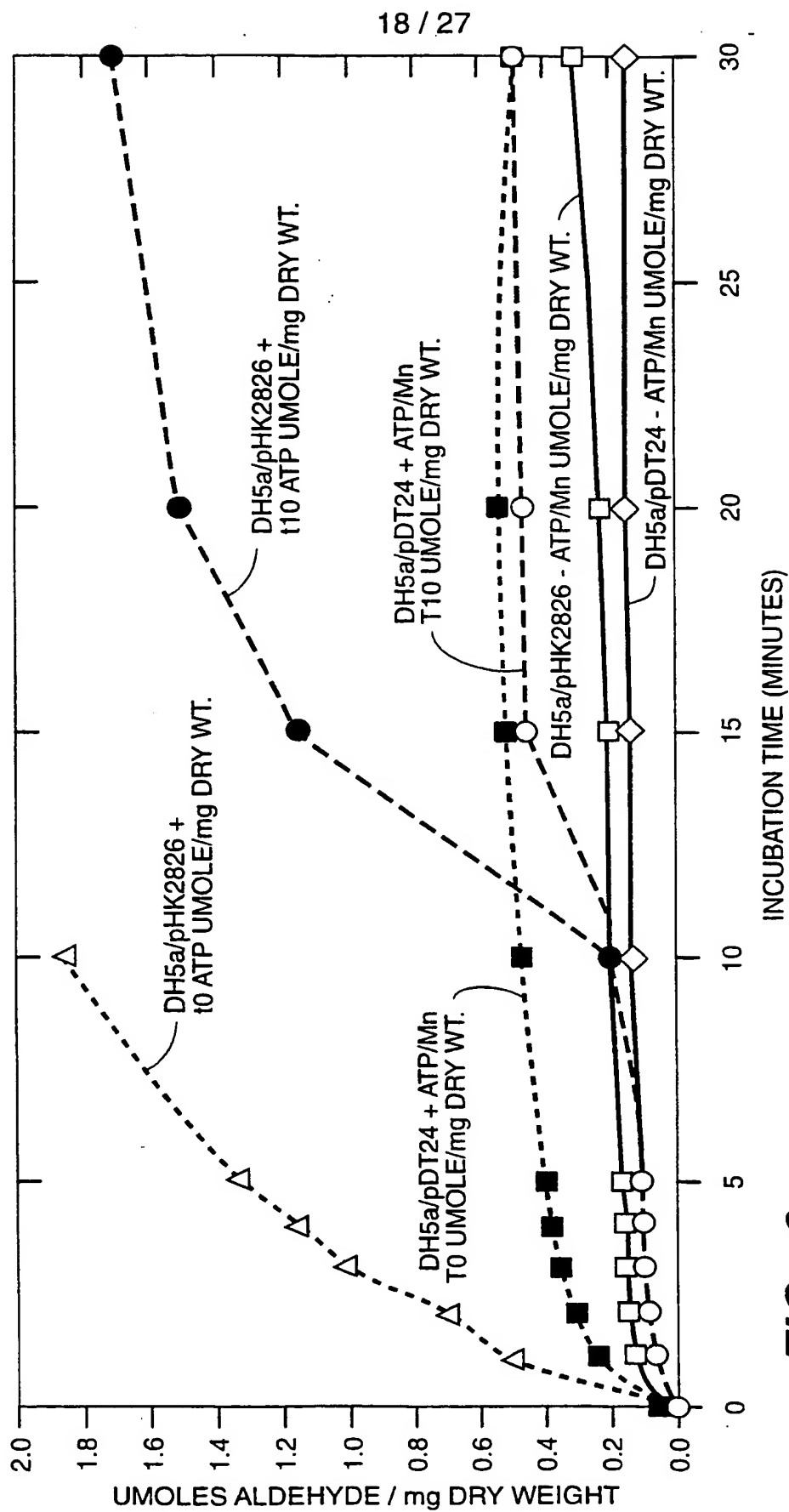


FIG. 6

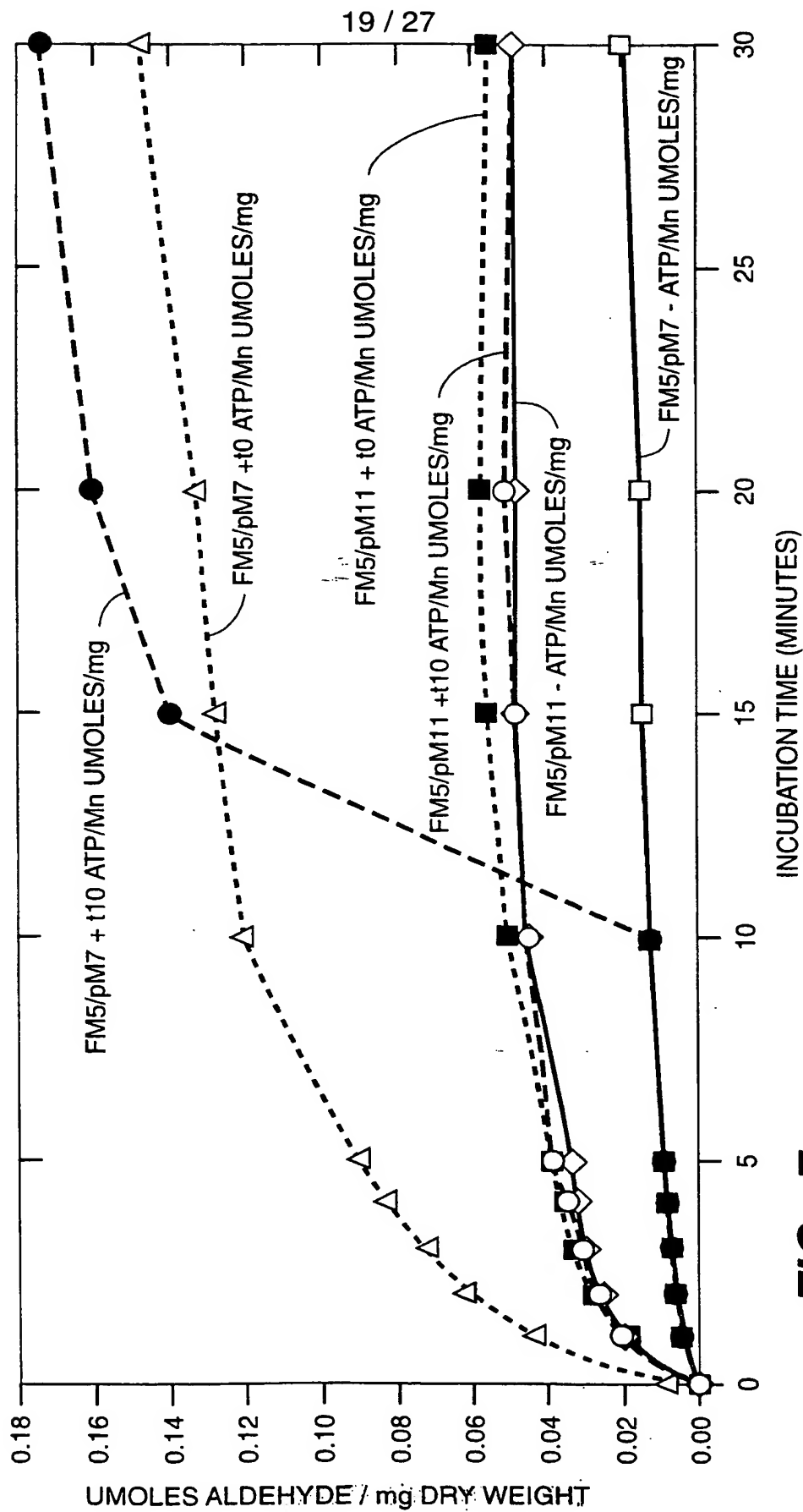


FIG. 7

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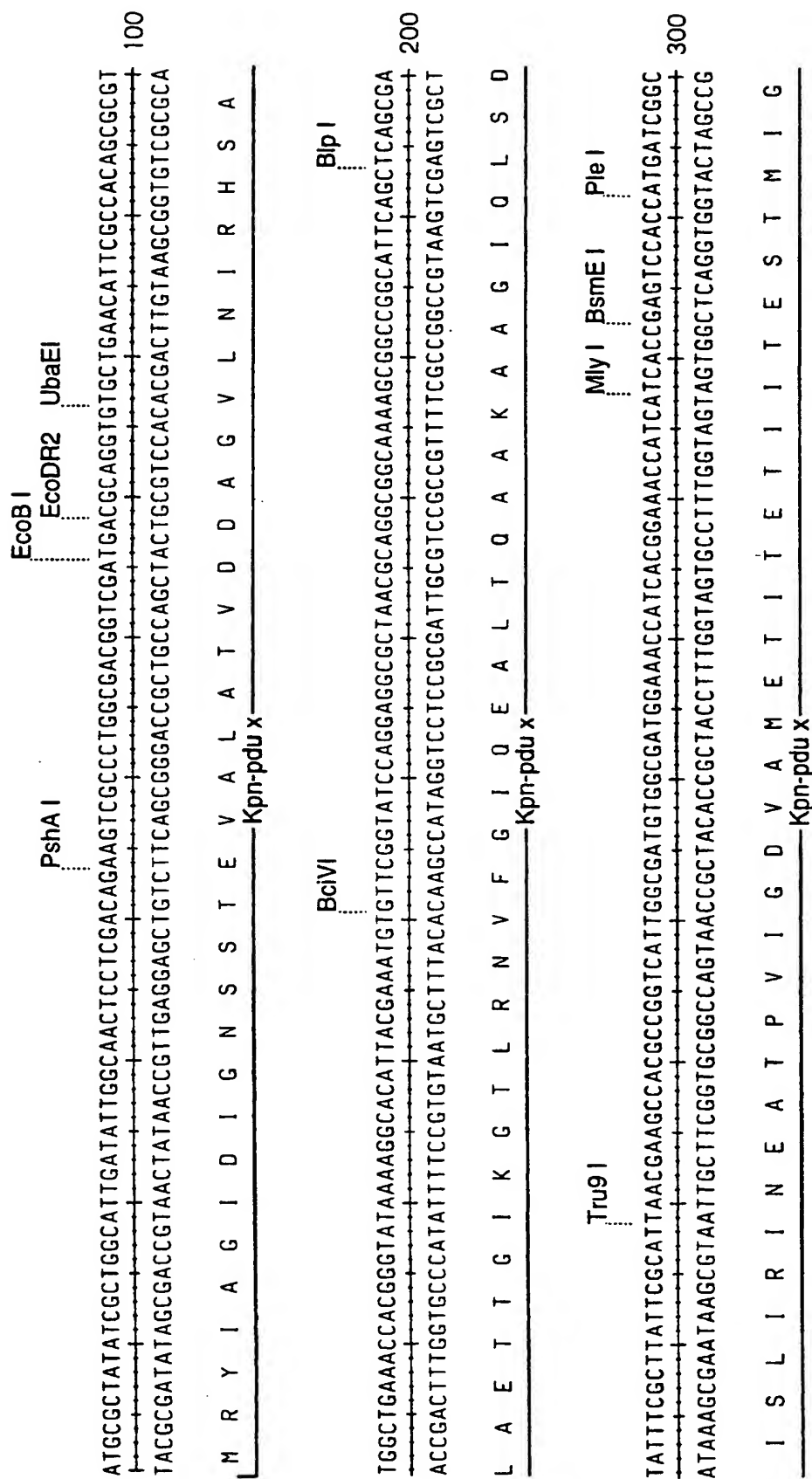


FIG. 8A-1

500

FIG. 8A-2

TGGTCTCCTCGGCCTTTGACCTTTGCCGATGTGCGCGCGATGGTCAATGCGGCAACGGCAGCGGGCTATCAGATAACCGGCATTATTTTGCAGCAGGATGA
 ACCAGAGGAGCGGAACTGAAACGGCTACAGCGGCGCTACCGGTACGCGGTGCGCGGATAGTCTAATGGCCGTAATAAAACGTCGTCCTACT
 V V S S A F D F A D V A A M V N A A T A A G Y O I T G I I L O O D D
 Kon-pdu x

FIG. 8B-1

GTGCTTTACCCGGTAAGATCATCGAAACGCTCTCAACCCCTTACGGTATTGGACCGTTTTCGATCTCAACGCCGAGGAGCCAAAATATCGTGCCAA 700
CAGCGAAATGGGCCATTCTAGTAGCTTTGGGAGAGGTTGGGAATGCCATAACGCTGGCAAAAGCTAGAGTTGCGGCTCCTCTCGGTTTTATAGCACGGTT
V I A L P G K I I E T L S N P Y G I A T V F D L N A E E S Q N I V P
Kpn-pdu x

M b i l B s r B I P p u 1253 I A a t II
TGGCACGGGCGCTGATTGGCAACCGCTCGGCCGTGGTGGAACCCCTCCGGCGACGTCAAGGCCCGCGCTATTCCGGCAGGTAATCTGTGCTCAT 800
ACCGTGCCCGCGACTAACCGTTGGCGAGCCGGCACCACCACCTTTTGGGGGAGGCCGCTGCAGTTCCGGGGCGGATAAGGCCGTCCTATTAGACAACGAGTA
M A R A L I G N R S A V V V K T P S G D V K A R A I P A G N L L L I
Kpn-pdu x

FIG._8B-2

A s p 16 H I C s p 6 I C v i R I I R s a I F s u I T t h 111 I
CGCTCAGGGGGCGCAGCGTACAGGTTGATGTGGCCCGCGGGCGGAGCCATCATGAAGCGGTGACGGCTGCGGCAACACGTCGCGGGAGAA 900
GCGAGTCCCGCGTGCATGTCCAACACCGGCGGCCCGCCCTTCGGTAGTACTTTTCGCCAACACGCGGACGCGGTTTGACCTGTTCAGCGGCCCTCTT
A Q G R S V O V D V A A G A E A I M K A V D G C G K L D N V A G E
Kpn-pdu x

FIG._8C-1

FIG. 8C-2

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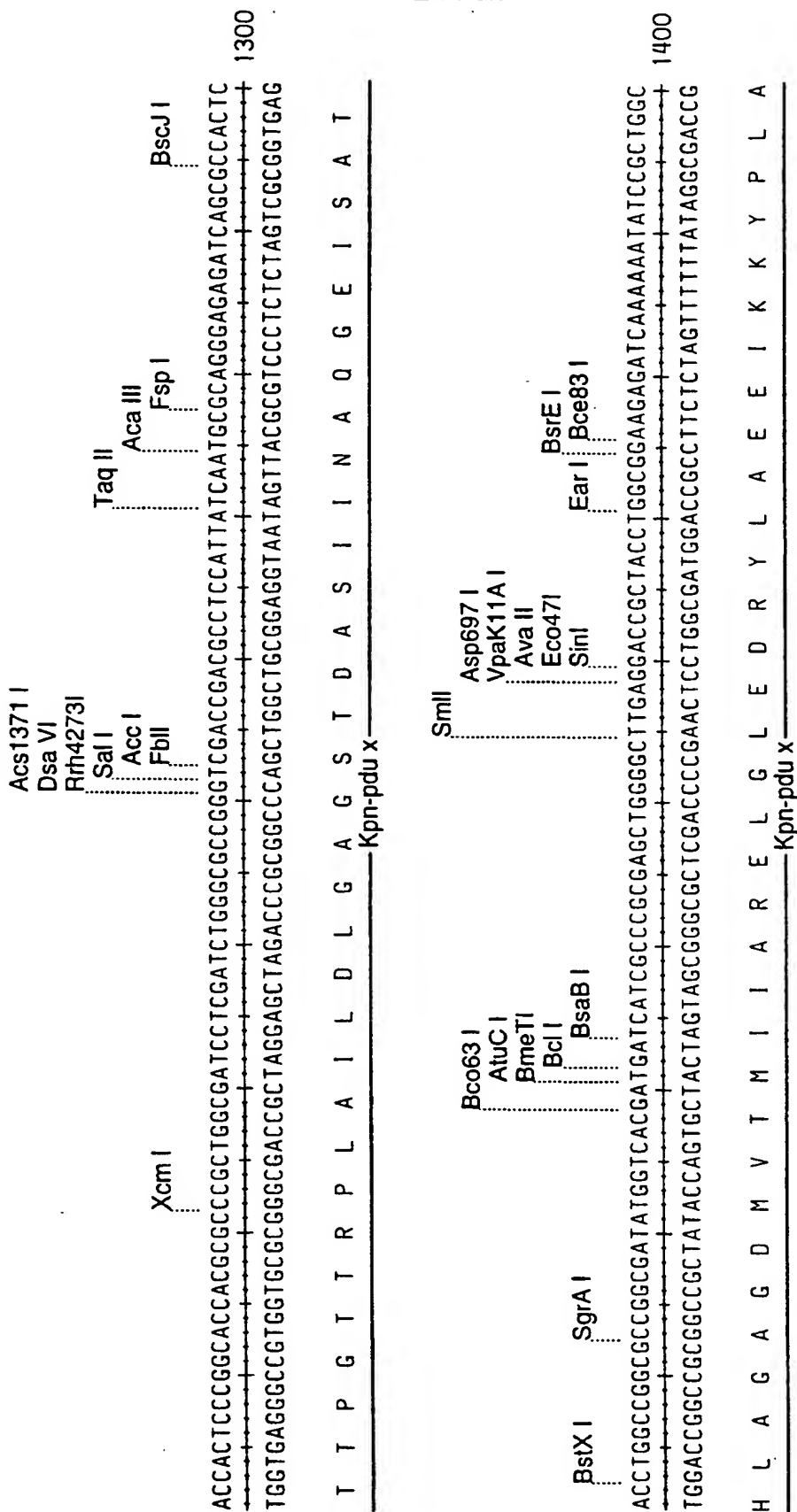


FIG._8D-1

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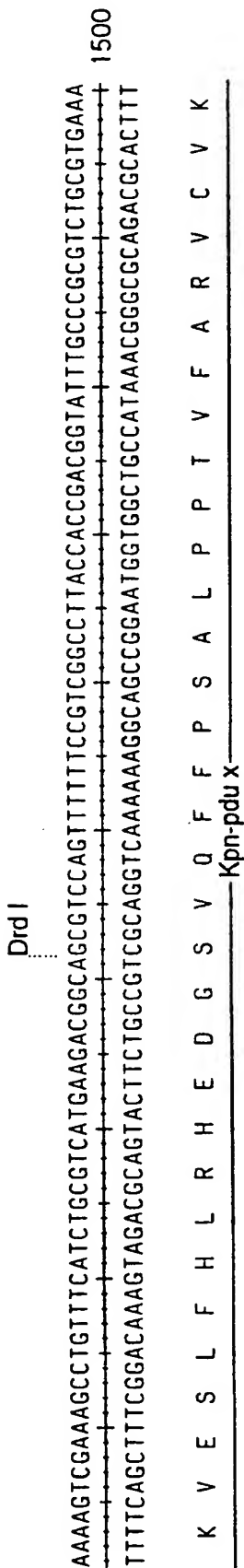


FIG._8D-2

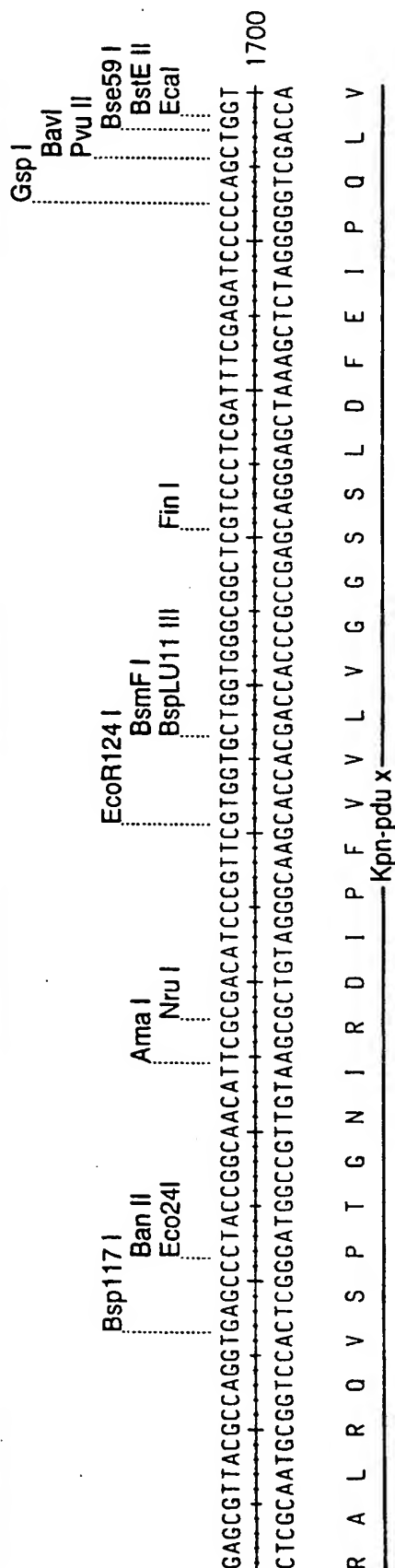
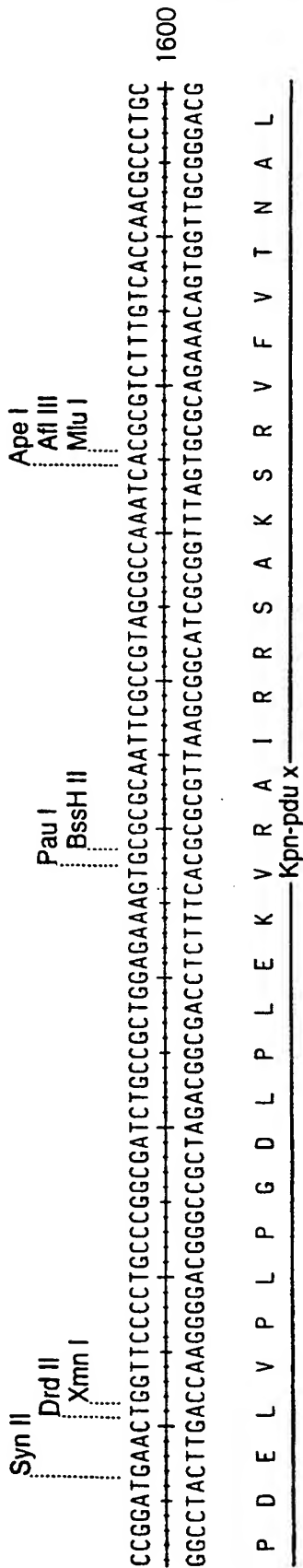


FIG._8E-1

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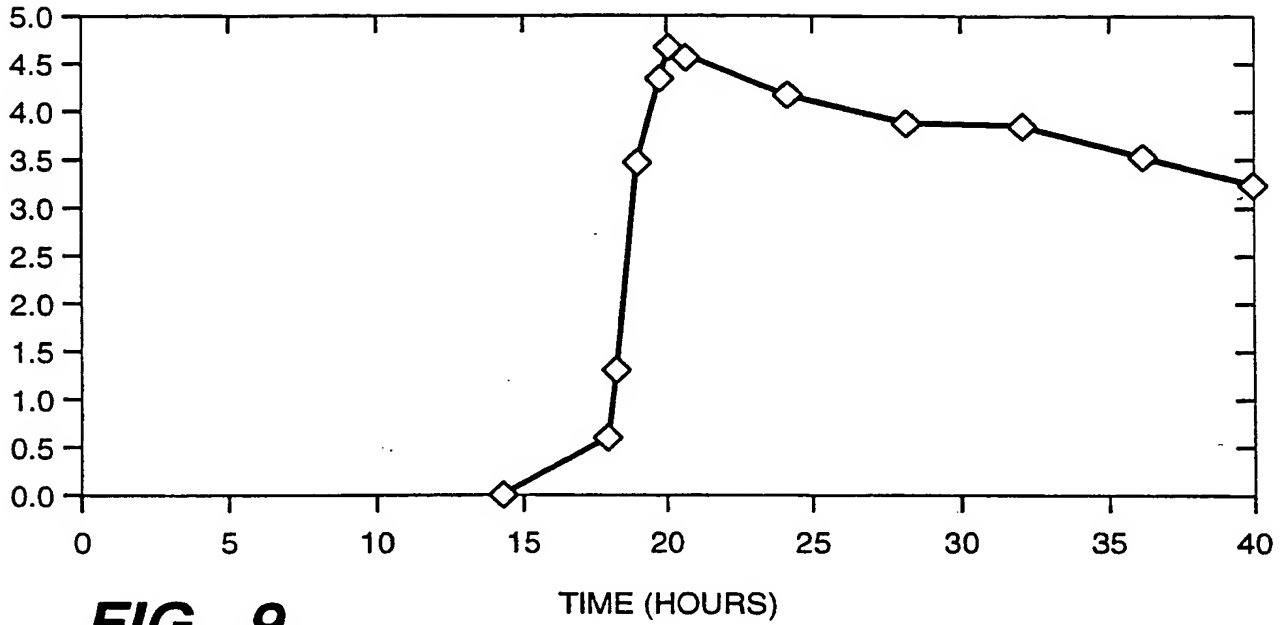
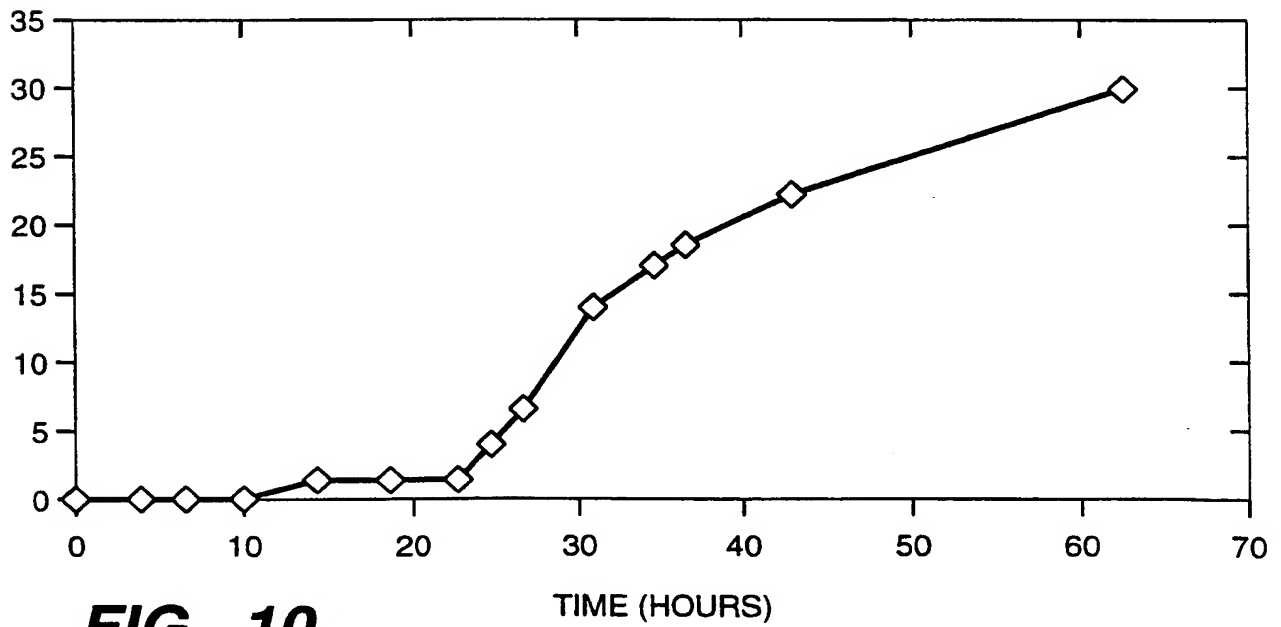
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 CACCGACGGCTGGCGCACTACCGGTGGTTGCCGGGCGGGCAACATCCGGGCTGTGAAGGCCACGCAATGCGGTGCGCCAGCGGATTACTCTTTCC
 GTGGCTGCGGACCGCGTGATGGCCGACCAACGGCCCGCGCGTTGTAGGCGCGGACACTTCGGGTGCGTTACGCCAGCGGTGCGCTAATGAGGAAAGG
 1800
 T D A L A H Y R L V A G R G N I R G C E G P R N A V A S G L L L S
 Kpn-pdu x

TGGCAAAAAGGAGGCACACATGGAGAGTAG
 ACCGTTTTTCCTCCGTGTGTACCTCTCATC
 1830

W O K G G T H G E
 Kpn-pdu x

FIG.-8E-2

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**FIG._9****FIG._10**